

SEQUENCE LISTING



(1) GENERAL INFORMATION:

(i) APPLICANT: Peter Ruhdal Jensen
Karin Hammer

(ii) TITLE OF INVENTION: Artificial promoter libraries for selected organisms and promoters derived from such libraries

(iii) NUMBER OF SEQUENCES: 58

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) CURRENT APPLICATION DATA:

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(B) FILING DATE: February 19, 1999

(vii) PRIOR APPLICATION DATA:

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(viii) ATTORNEY/AGENT INFORMATION:

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(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

B1

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:26..82

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION:/evidence= EXPERIMENTAL /standard_name="Artificial promoter library" /note= "A degenerated sequence specifying a mixture of artificial promoters covering a wide range of expression in small steps in *L. lactis*"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION:31..45

(D) OTHER INFORMATION:/standard_name= "Consensus sequence"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION:60..69

(D) OTHER INFORMATION:/standard_name= "Consensus sequence"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION:74..82

(D) OTHER INFORMATION:/standard_name= "Consensus sequence"

(ix) FEATURE:

(A) NAME/KEY: -35_signal

(B) LOCATION:40..45

(D) OTHER INFORMATION:/standard_name= "-35 box"

(ix) FEATURE:

(A) NAME/KEY: -10_signal

(B) LOCATION:63..68

(D) OTHER INFORMATION:/standard_name= "Pribnow box"

(ix) FEATURE:

(A) NAME/KEY: misc_recomb

(B) LOCATION:3..25

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION:/evidence= EXPERIMENTAL /standard_name="Multiple cloning site" /label= MCS
/note= "A sequence specifying recognition sites for the restriction endonucleases: *Nla*IV, *Bst*YI, *Bam*HI, *Alw*I, *Mbo*I, *Dpn*I, *Afl*II, *Mse*I, *Ssp*I, *Nsi*I."

(ix) FEATURE:

(A) NAME/KEY: misc_recomb

(B) LOCATION:74..98

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION:/evidence= EXPERIMENTAL /standard_name="Multiple cloning site"
/label= MCS
/note= "A sequence specifying recognition sites for the restriction endonucleases: *Sca*I, *Rsa*I, *Hpa*I, *Hinc*II, *Mse*I, *Sfc*I, *Pst*I, *Fnu*4HI, *Bbv*I, *Pvu*II, *Nsp*BII, *Alu*I, *Eco*RI."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGGGATCCTT AAGAATATTA TGCATNNNNN AGTTTATTCT TGACANNNNN NNNNNNNNNT 60
GGTATAATAN NANAGTACTG TTAAGTGCAG CTGAATTCGG 100

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:23..95
- (D) OTHER INFORMATION:/standard_name=

"Artificial promoter library"
/note= "A degenerated sequence specifying a mixture of
artificial temperature regulated promoters covering a wide range of
expression in small steps in *L. lactis*"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:23..49
- (D) OTHER INFORMATION:/standard_name=

"Sequence providing temperature regulation to promoters"
/note= "This sequence comprising two inverted repeats
separated by a short spacer provides temperature (heat shock) regulation to
promoters in Gram-positive bacteria"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:50..60
- (D) OTHER INFORMATION:/standard_name=

"Consensus sequence"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:75..84
- (D) OTHER INFORMATION:/standard_name= "Consensus sequence"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:89..95
- (D) OTHER INFORMATION:/standard_name= "Consensus sequence"

(ix) FEATURE:

- (A) NAME/KEY: -35_signal
- (B) LOCATION:55..60
- (D) OTHER INFORMATION:/standard_name= "-35 box"

(ix) FEATURE:

- (A) NAME/KEY: -10_signal
- (B) LOCATION: 78..83
- (D) OTHER INFORMATION: /standard_name= "Pribnow box"

(ix) FEATURE:

- (A) NAME/KEY: misc_recomb
- (B) LOCATION: 3..22
- (D) OTHER INFORMATION: /standard_name= "Multiple cloning site"
/label= MCS
/note= "A sequence specifying recognition sites for the restriction endonucleases: NlaIV, BstYI, BamHI, AlwI, MboI, DpnI, HindIII, AluI, MseI (2 sites), SspI, AseI."

(ix) FEATURE:

- (A) NAME/KEY: misc_recomb
- (B) LOCATION: 89..111
- (D) OTHER INFORMATION: /standard_name= "Multiple cloning site"
/label= MCS
/note= "A sequence specifying recognition sites for the restriction endonucleases: ScaI, RsaI, SfcI, PstI, Fnu4HI, BbvI, PvuII, NspBII, AluI, XbaI, MaeI, EcoRI, ApoI."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CGGGATCCAA GCTTAATATT AATTAGCACT C>NNNNNNNNN GAGTGCTAAT TTTTGTGACA 60
NNNNNNNNNN NNNNTGGTAT AATANNANAG TACTGCAGCT GTCTAGAATT CGG 113

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: protein_bind
- (B) LOCATION: 10..16
- (D) OTHER INFORMATION: /function= "Activating promoters in *S. cerevisiae*"
/bound_moiety= "GCN4 protein"
/standard_name= "Upstream activating sequence" /label= UAS_GC4p
/note= "A DNA sequence that specifies a binding site for the GCN4 protein, which activates the transcription of genes involved in amino acid synthesis in *S. cerevisiae*."

(ix) FEATURE:

(A) NAME/KEY: TATA_signal
 (B) LOCATION:67..72
 (D) OTHER INFORMATION:/standard_name= "TATA box"

(ix) FEATURE:
 (A) NAME/KEY: misc_signal
 (B) LOCATION:122..144
 (D) OTHER INFORMATION:/function= "Transcription initiation"
 /standard_name= "TI box"

(ix) FEATURE:
 (A) NAME/KEY: protein_bind
 (B) LOCATION:122..144
 (D) OTHER INFORMATION:/bound_moiety= "Arginine repressor"
 /standard_name= "arginine repressor binding site"
 /label= argR

(ix) FEATURE:
 (A) NAME/KEY: misc_RNA
 (B) LOCATION:145..192
 (D) OTHER INFORMATION:/function= "Spacer"
 /standard_name= "Part of native sequence for ARG8 gene incl. first codon"

(ix) FEATURE:
 (A) NAME/KEY: misc_recomb
 (B) LOCATION:3..8
 (D) OTHER INFORMATION:/standard_name= "Recognition site for restriction endonuclease EcoRI"
 /label= EcoRI_site

(ix) FEATURE:
 (A) NAME/KEY: misc_recomb
 (B) LOCATION:192..197
 (D) OTHER INFORMATION:/standard_name= "Recognition site for restriction endonuclease BamHI"
 /label= BamHI_site

(ix) FEATURE:
 (A) NAME/KEY: promoter
 (B) LOCATION:10..192
 (D) OTHER INFORMATION:/standard_name= "Artificial promoter library"
 /note= "A degenerated sequence specifying a mixture of artificial promoters covering a wide range of expression in small steps in *S. cerevisiae*"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CAGAATTCGT GACTCANNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 60
 NNNNNNNNNN NNNNNNTATA AANNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 120
 NCTCTTAAGT GCAAGTGACT GCGAACATTT TTTTCGTTTG TTAGAATAAT TCAAGAATCG 180
 CTACCAATCA TGGATCCCG 199

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas putida*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:1..45
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/evidence= EXPERIMENTAL /standard_name="Artificial promoter library" /note= "A degenerated sequence specifying a mixture of artificial promoterscovering a wide range of expression in small steps *Pseudomonas putida*"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

NNNNNNNNTT GRNNNNNNNNN NNNNNNNNNNN NTATRATNNN NNNNN

45

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:4..60
- (D) OTHER INFORMATION:/standard_name= "Constitutional promoter" /label= Cp1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CATACCGGAG TTTATTCTTG ACAGTTCAC CTCGGGTGA TATAATATCT CAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Lactococcus lactis
- (ix) FEATURE:
 - (A) NAME/KEY: promoter
 - (B) LOCATION:4..60
 - (D) OTHER INFORMATION:/standard_name= "Constitutional promoter"
/label= Cp10
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CATGGCTTAG TTTATTCTTG ACAGGGTAGT ATCACTGTGA TATAATAGGA CAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Lactococcus lactis
- (ix) FEATURE:
 - (A) NAME/KEY: promoter
 - (B) LOCATION:4..59
 - (D) OTHER INFORMATION:/standard_name= "Constitutional promoter"
/label= Cp11
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CATAAGTGAG TTTATTCTTG ACCCGGACGC CCCCTTTGA TATAATAAGT AGTACTGTT 59

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Lactococcus lactis
- (ix) FEATURE:
 - (A) NAME/KEY: promoter
 - (B) LOCATION:4..60
 - (D) OTHER INFORMATION:/standard_name= "Constitutional promoter"
/label= Cp12
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CATATACAAG TTTATTCTTG ACACTAGTCG GCCAAAATGA TATAATACCT GAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Lactococcus lactis
- (ix) FEATURE:
 - (A) NAME/KEY: promoter
 - (B) LOCATION:4..60
 - (D) OTHER INFORMATION:/standard_name= "Constitutional promoter"
/label= Cp13
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CATGCTTTAC TTTATTCTTG ACAAACCAC CAGCTTTTGG TATAATACGT GAGAACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name= "Constitutional promoter"
/label= Cp14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CATGACGGAG TTTATTCTTG ACACAGGTAT GGACTTATGA TATAATAAAA CAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name= "Constitutional promoter"
/label= Cp15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CATTACNTAG TTNATTCTTG ACAGAATTAC GATTCGCTGG TATAATATAT CAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:4..58
- (D) OTHER INFORMATION:/standard_name= "Constitutional promoter"
/label= Cp16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CATTGTGTAG TTTATTCTTG ACAGCTATGA GTCAATTGG TATAATAACA GTACTCAG 58

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:4..59
- (D) OTHER INFORMATION:/standard_name= "Constitutional promoter"
/label= Cp17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CATTCTGGAG TTTATTCTTG ACCGCTCAGT ATGCAGTGGT ATAATAGTAC AGTACTGTT 59

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:4..58

(D) OTHER INFORMATION:/standard_name= "Constitutional promoter"
/label= Cp18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CATTTTGCAG TTTATTCTTG ACATTGTGTG CTTCGGGTGT ATAATACTAA GTACTGTT 58

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:4..58
- (D) OTHER INFORMATION:/standard_name= "Constitutional promoter"
/label= Cp19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CATCGCTTAG TTTTCTTGA CAGGAGGGAT CCGGGTTGAT ATAATAGTTA GTACTGTT 58

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:4..60
- (D) OTHER INFORMATION:/standard_name= "Constitutional promoter"
/label= Cp2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CATTGCTAG TTTATTCTTG ACATGAAGCG TGCCTAATGG TATATTACTT GAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:4..60
- (D) OTHER INFORMATION:/standard_name= "Constitutional promoter"
/label= Cp20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CATGGGTGAG TTTATTCTTG ACAGTGC GGC CNGGGGCTGA TATCATAGCA GAGTACTATT 60

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:4..59
- (D) OTHER INFORMATION:/standard_name= "Constitutional promoter"
/label= Cp21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CATTACCGAG TTTATTCTTG ACACCGTTTA TCGGGGTTGT ATAATACTAT AGTACTGTT 59

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:4..60
- (D) OTHER INFORMATION:/standard_name= "Constitutional promoter"
/label= Cp23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CATGTAGGAG TTTATTCTTG ACAGATTAGT TAGGGGGTGG TATAATATCT CAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:4..60
- (D) OTHER INFORMATION:/standard_name= "Constitutional promoter"
/label= Cp24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CATGGGTAAG TTTATTCTTC ACACTATCTG GGCCCGATGG TATAATAAGT GACTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:3..59

(D) OTHER INFORMATION:/standard_name= "Constitutional promoter"
/label= Cp25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CTTTGGCAGT TTATTCTTGA CATGTAGTGA GGGGGCTGGT ATAATCACAT AGTACTGTT 59

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name= "Constitutional promoter"
/label= Cp26

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CATTCTACAG TTTATTCTTG ACATTGCACT GTCCCCCTGG TATAATAACT ATACATGCAT 60

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CATGGGGCCG TTTATTCTTG ACAACGGCGA GCAGACCTGG TATAATAATA TAGTACTGTT

60

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..59

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp29

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CATCGGTAAG TTATTCTTGA CATCTCAGGG GGGACGTGGT ATAATAACTG AGTACTGTT

59

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CATCCTGTAG TTTATTCTTG ACACACGTNN TTAGCTGTGG TATAATAGGA GAGTACTGTT

60

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CATGACAGAG TTTATTCTTG ACAGTATTGG GTTACTTTGG TATAATAGTT GAGTACTGTT

60

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp32

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CATACGGGAG TTTATTCTTG ACATATTGCC GGTGTGTTGG TATAATAACT TAGTACTGTT

60

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CATGTTGGAG TTTATTCTTG ACATACAATT ACTGCAGTGA TATAATAGGT GAGTACTGTT

60

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp34

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CATCGCGAAG TTTATTCTTC ACACACCGCA GAACTTGTGG TATAATACAA CAGTACTGTT

60

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..59

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp37

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CATCATTAAG TTTATTCTTC ACATTGGCCG GAATTGTTGT ATAATACCTT AGTACTGTT

59

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp38

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CATAGAGAAG TTTATTCTTG ACAGCTAACT TGGCCTTTGA TATAATACAT GAGTACTGTT

60

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

CATTGCGAAG TTTATTCTTG ACAGTACGTT TTTACCATGA TATAATAGTA TAGTACTGTT

60

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GATGTTTTAG TTTATTCTTG ACACCGTATC GTGCGCGTGA TATAATCGGG ATCCTTAAGA

60

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CATAGAACAG TTTATTCTTG ACATTGAATA AGAAGGCTGA TATAATAGCC AGTACTGTT

59

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp41

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CATCCGCAAG TTTATTCTTG ACAGCTGAAT GTAGACGTGG TATAATAGTT AAGTACTGTT

60

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

CATTCGTAAG TTTATTCTTG ACACCTGAGA TGAGGCGTGA TATAATAAAT AAGTACTGTT

60

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..59

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp44

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CATCGGGTAG TTTATTCTTG ACAATTAAGT AGAGCCTGAT ATAATAGTTC AGTACTGTT

59

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..59

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION:/evidence= EXPERIMENTAL
/standard_name= "Constitutional promoter"
/label= Cp5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CATGGGGGAG TTTATTCTTG ACATCATCTT CGTAGCCTGG TATACTACAT GAGTATGTT

59

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CATGTGGGAG TTTATTCTTG ACACAGATAT TTCCGGATGA TATAATAACT GAGTACTGTT

60

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

TATGCGGTAG TTTATTCTTG ACATGACGAG ACAGGTGTGG TATAATGGGT CTAGATTAGG

60

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

CATTCTTTAG TTTATTCTTG ACAAACGTAT TGAGGACTGA TATAATAGGT GAGTACTGTT

60

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard_name= "Constitutional
promoter"
/label= Cp9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CATAGTCTAG TTTATTCTTG ACACGCGGTC CATTGGCTGG TATAATAATT TAGTACTGTT

60

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 8..177

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/standard_name= "Yeast promoter"

/label= Yp102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GAATTCGTGA CTCAAACGGG TGGTCGACGG GTGGTTCCAA TTAATTGGCG TCCCTCTTAT	60
AAAGGCGAGG GTACGTGCGA CAATTGGTAG AGCGAGCGGG GCTCTTAAGT GCAAGTGACT	120
GCGAACATTT TTTTCGTTTG TTAGAATAAT TCAAGAATCG CTACCAATCA TGGATCC	177

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 8..181

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/standard_name= "Yeast promoter"

/label= Yp112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GAATTCGTGA CTCACGGCAT CTGATGGTTG ACCATAGTCA GGAACATTGT GCTGGAGTTC	60
CTTGAGGAAT GAGTTATAAA ATGGGAGGTT GCGGCTAATG CCAGGCAGGA GAGGAACCCT	120
CTTAAGTGCA AGTGACTGCA AACATTTTTT TCGTTTGTTG AATCGCTACC AATCATGGAT	180
CC	182

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 191 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Saccharomyces cerevisiae*
- (ix) FEATURE:
 - (A) NAME/KEY: promoter
 - (B) LOCATION: 8..181
 - (C) IDENTIFICATION METHOD: experimental
 - (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp13
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GAATTCGTGA CTCACTAGGC AGGTCACGTT GGCTCTTCGC GGC GCAGGTT CGTATGCCGC	60
GCCGCCAGGG GCTTTATAAA GGTCGTCCTG GGTACAGTTG GGATGGCTCC ACGTTTCGGC	120
TCTTAAGTGC AAGTGACTGC GAACATTTTCG TTTGTTAGAA TAATTCAAGA ATCGCTACCA	180
ATCATGGATC C	191

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 167 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Saccharomyces cerevisiae*
- (ix) FEATURE:
 - (A) NAME/KEY: promoter
 - (B) LOCATION: 8..167
 - (C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION:/evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GAATTCGTGA CTCAGGGCCG TACTAAGTAG CTTTCGTATG CTATGCGGGG TTTTATAAAT	60
CTTTGGGCCA TGGTCTTGCT GGAAACACC TCTCTTAAGT GCAAGTGACT GCGAACATTT	120
TTTTCGTTTG TTAGAATAAT TCAAGAATCG CTACCAATCA TGGATCC	167

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 8..191
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GAATTCGTGA CTCACCGCTC GGGTGCAGGG CCAAGGCGGC GGAATGTGCG GGGCGTTCTA	60
GCGCAATCGG GGTATAAATT TATAAGGAGG CTGCGGGTGC TAGTTTGTCT AGTTTGACTC	120
TTAAGTGCAA GTGACTGCGA ACATTTTTCG TTTGTTAGAA TAATTCAAGA ATCGCTACCA	180
ATCATGGATC C	191

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 8..190

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/standard_name= "Yeast promoter"

/label= Yp18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

GAATTCGTGA CTCAGGATTA GCTATGCCGG TTGGGATAAG CGAACAACTG GAGGTGAGAA	60
GCTTTTTGTC AGAATATAAA CCCGTTAGTC AGGGTTTGGT GGGATAGGGG GTACTGTACC	120
TCTTAAGTGC AAGTGA CTGC GAACATTTTT TTCGTTTGGT AGAATAATTC AAGAATCGCT	180
ACCAATCATG GATCC	195

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 8..179

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/standard_name= "Yeast promoter"

/label= Yp183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GAATTCGTGA CTCACTAAGG GTTCGCCATT AACAGAATCG CTGGTAGAAC ATCGGTAGTT	60
AGGCACCCGA GTATAAACAG GCGGACCCCT CACGGATATC AGCTGATAGT GCGAGCCTCA	120

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Saccharomyces cerevisiae*
- (ix) FEATURE:
 - (A) NAME/KEY: promoter
 - (B) LOCATION: 8..190
 - (C) IDENTIFICATION METHOD: experimental
 - (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yest promoter"
/label= Yp190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

GAATTCGTGA CTCAGTATCC ACGGGTGTTT GAGGGCTGGT CGCAGGTTAG CAGGCGAGGG	60
CGGGTGTTTA CGGCTATAAA TGAGTGTGTTG CAGCCGGGTA CGGGCGTACG AGTAGTGATC	120
TCTTAAATGC AAGTGACTGC GAACATTTTTT TTCGTTTGTT AGAATAATTC AAGAATCGCT	180
ACCAATCATG GATCC	195

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Saccharomyces cerevisiae*
- (ix) FEATURE:
 - (A) NAME/KEY: promoter

(B) LOCATION:8..189
(C) IDENTIFICATION METHOD: experimental
(D) OTHER INFORMATION:/evidence= EXPERIMENTAL
/standard_name= "Yest promoter"
/label= Yp191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GAATTCGTGA CTCAATGCTG CGGGCGGCAG GAGTCTGGTG TAACTTCCCA TTTTGAGTGA	60
AAGACAGACC ATCTATAAAC ATTTGGTGGG CAAAGTGGCC TGGCGGATTT GTTTGGACTC	120
TTAAGTGAAA GTGACTGCGA ACATTTTTTTT CGTTTGTTAG AATAATTCAA GAATCGCTAC	180
CAATCATGGA TCC	193

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

(A) NAME/KEY: promoter
(B) LOCATION:8..166
(C) IDENTIFICATION METHOD: experimental
(D) OTHER INFORMATION:/evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

GAATTCGTGA CTCACTTAAG GCTACTGCGG AAGTTTAGAT CTAAGGTCGG AAATAATTTA	60
GAAAATTACG ACATTATAAA TAGCGGAGAG GCCAGGTGAT GGGCACCATT GTGGGGGGGC	120
TCTTAATTGT TAGAATAATT CAAGAATCGC TACCAATCAT GGATCC	166

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:
(A) NAME/KEY: promoter
(B) LOCATION: 8..190
(C) IDENTIFICATION METHOD: experimental
(D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GAATTCGTGA CTCAGTCGCC CGCAAGATGG GATGGTGCAT TTAAACACC CGAATTATAC	60
TCGTCAACTT ATAGTATAAA CGGAACGCGA CGATACGTC TAGTTTTTCGG CGAAGTCGAC	120
TCTTAAGTGC AAGTGA CTGC GAACATTTTTT TTCGTTTGT AGAATAATTC AAGAATCGCT	180
ACCAATCATG GATCC	195

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:
(A) NAME/KEY: promoter
(B) LOCATION: 8..183
(C) IDENTIFICATION METHOD: experimental
(D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

GAATTCGTAC TCACGACAGC GTTATGACTT CGAGGACCAG CTA CTCCGG TCGCGTACTA	60
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GTTTTTACCT GTATAAACTT TGCTACCGCT GGGCCTTGGT GGTGCTGTCC CGCTCTTAAG	120
TGCAAGTGAC TGCGAACATT TTTTTCGTTT GTTACAATAA TTCAAGAATC GCTACCAATC	180
ATGGATCC	188

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Saccharomyces cerevisiae*
- (ix) FEATURE:
 - (A) NAME/KEY: promoter
 - (B) LOCATION: 8..190
 - (C) IDENTIFICATION METHOD: experimental
 - (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GAATTCGTGA CTAAATGGAT AAGGTTATCG CCATCACGGA GTCTTCTCTC ACGTCTGGAG	60
CAGAGGCTAG ACCTTATAAA TTATACATGG TGGGAGAGGC GATAGTCTTT AGAGACGTGC	120
TCTTAAGTGC AAGTGACTGC GAACATTTTT TTCGTTTGTT AGAATAATTC AAGAATCGCT	180
ACCAATCATG GATCC	195

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 189 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 8..184
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```
GAATTCGTGA CTCACAAGAA TGTGGGCGGG TCGTTAAACT GAGCCTGGAC ACCTTGGCTG      60
CGTCGCTTTC GTATAAAGAT CTTAGAGCTG TGGAGTCTGG GTCGAGTGGC CAGCTCTTAA    120
ATGCAAGTGA CTGCGAACAT TTTTTCGTT TGTTAGAATA ATTCAAGAAT CGCTACCAAT    180
CATGGATCC                                     189
```

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 8..190
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```
GAATTCGTGA CTCACTCGGA AGATTGGGTT TACGATTAGG ATGGCGCGGC AGAACCGGGG      60
GGGATTCCCT TCTATATAAA GGGTTCCGAT ACTACGTGCT GCGGACGGCC GATCGAGTTA    120
TCTTAAGTGC AAGTGACTGC GAAAAATTTT TTCGTTTGTT AGAATAATTC AAGAATCGCT    180
ACCAATCATG GATCC                                     195
```

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 8..171
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL
/standard_name= "Yeast promoter"
/label= Yp96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

B1
Cont

GAATTCGTGA CTCATCTAGT GAGAGGAGCC GTGGTATCTT GTGTCACCAC CAGGGGAAAA	60
TAATGGCAGG GGTGTATAAA TGGTCGAGTA GTCGCGACCC ACGCTGCAAG GCAAGGAACT	120
CTTAAATTTT TTTCGTTTGT TAGAATAATT CAAGAATCGC TACCAATCAT GGATCC	176
